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FIGURE 298

MKDMPLRIHVLLGLAITTLVQAVDKKVCPRCTCEIRPWFTPRSIYMEASTVDCNDLGLLTF
PARLPANTQILLQTNNIAKIEYSTDFPVNLTGDLDSQNNLSSVTNINVKKMPQLLSVYLEEN
KLTPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLLRLHLNSNRLQMINSKWFDALPN
LEILMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLLENLEISFYDNRLIKVP
HVALQKVVNLFKLDLNKNPINRIRRGDFSNNMLHLKELGINNMPELISIDSLAVDNLPLDKIE
ATNNPRLSYIHPNAFFRLPKLESLMLNSNALSALYHGTTIESLPNLKEISIHNPIRCDCVIRW
MMNMKTNIRFMEPDSLFCVDPPEFQGGQNVQRVHFRDMMEICPLIAPESFPSNLNVEAGSYVS
FHCRAEAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLDINGVTPKEGGLYTCIATNLVGA
DLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFAVKTENSHAAQ
SARIPSDVKVYNLTHLNPSTYEYKICIDIPTIYQKNRKKCVNVTTKGLHFDQKEYEKNNTTLM
ACLGGLLGIIGVICLISCLSPENMCDGGHSYVRNYLQKPTFALGELYPPPLINLWEAGKEKSTS
LKVKATVIGLPTNMS

Important features:**Signal sequence:**

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629**Casein kinase II phosphorylation site.**

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708**Cell attachment sequence.**

amino acids 277-280

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FIGURE 299

GCTGTGGGAACCTCTCCACGCGCACGAACCTCAGCCAACGATTTCGTGATAGATTTTGGGAGTT
TGACCAGAGATGCAAGGGGTGAAGGAGCGCTTCCTACCGTTAGGGAACTCTGGGGACAGAGCG
CCCCGCGCGCTGATGGCCGAGGCAGGGTGCACCAGGACCCAGGACGGCGTCGGGAACCAT
ACCATGCCCCGGATCCCCAAGACCCATAAGTTCTGTCGTCTCATCGTCGCGGTCTGCTGCCA
GTCTCTAGCTTACTCTGCCACCACTGCCCGGCAGGAGGAAGTCCCCAGCAGACAGTGGCCCCA
CAGCAACAGAGGCACAGCTTCAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAACAT
ACTGGAGCCTGTAAACCGTGCACAGAGGGTGTGGATTACACCACGCTTCCAACAATGAACCT
TCTTGCTTCCCATGTACAGTTTGTAAATCAGATCAAAAACATAAAAGTTCTTGCACCATGACC
AGAGACACAGTGTGTCAGTGTAAAGAAGGCACCTTCCGGAATGAAAACCTCCCAGAGATGTGC
CGGAAGTGTAGCAGGTGCCCTAGTGGGGAAGTCCAAGTCAGTAATTGTACGTCCTGGGATGAT
ATCCAGTGTGTTGAAGAATTTGGTGCCAATGCCACTGTGAAAACCCAGCTGCTGAAGAGACA
ATGAACACCAGCCCCGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGAACACCAGCCCAGGG
ACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCCGGGACTCCTGCCCCAGCTGCT
GAAGAGACAATGACCACCAGCCCCGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACC
AGCCCCGGGACTCCTGCCTCTTCTCATTACCTCTCATGCACCATCGTAGGGATCATAGTTCTA
ATTGTGCTTCTGATTGTGTTTGTTGAAAGACTTCACTGTGGAAGAAATTCCTTCCTTACCTG
AAAGGTTCAAGTAGGCGCTGGCTGAGGGCGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCT
CTGCTGTGTTCCACAGACAGAAACGCCTGC

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FIGURE 300

MARIPKTLKFVVVIVAVLLPVLAYSATTARQEEVPQQTVA PQQQRHSFKGEECPAGSHRSEHT
GACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKS SCTMTRDTVCQCKEGTFRNENSPEMCR
KCSRCPSGEVQVSNCTSWDDIQCVEEFGANATVETPAAEETMNTSPGTPAPAAEETMNTSPGT
PAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPASSHYLSCTIVGIIVLI
VLLIVFV

Important features:**Signal peptide:**

Amino acids 1-29

Transmembrane domain:

Amino acids 240-259

N-glycosylation site:

Amino acids 77-81;140-144;156-160

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 126-130

N-myristoylation sites:

Amino acids 56-62;72-78;114-120;154-160;233-239

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FIGURE 301

CACAAGCATCTTAATTTGAATCCACAAAGTTTCATGTAATGAAAAGAAATACATAATTTTAAT
TCAACCCGAGTGTTTTCCAAGAAGATTGTATTTGCTTAAATTGCTACAGTAATTCAGAGACA
GCCCTGTCTGGACACAGAGTTTACTGTGGATTTTTAAGAGACTCAGTTAAAGAATTTAGGAATT
TCTGATTCATTTAAAGGATTTACAAATTCATCAACCCCTGAAAACCTAAAGCAAATGAACAGG
AAAAAAAAAAGAAGATGGGTTTTTAAGTCCAATATATGTTATTTTCTTCTTTTTTGGAGTC
AAAGTACATTGCCAATATGAACTTATCAGTGGGATGAAGACTATGACCAAGAGCCAGATGAT
GATTACCAAACAGGATTTCCATTTTCGTCAAATGTAGACTACGGAGTTCCTTTTCATCAGTAT
ACTTTAGGCTGTGTCAAGTGAATGCTTCTGTCCAATACTTTCCATCATCAATGTACTGTGAT
AATCGCAAATCAAGACTATCCCAAATATTCCGATGCACATTGAGCAACTCTACCTTCAGTTC
AATGAAATTGAGGCTGTGACTGCAAATTCATTTCATCAATGCAACTCATCTTAAAGAAATTAAC
CTCAGCCACAACAAATTAATCTCAAAGATTGATTATGGTGTGTTTGCTAAGCTTCCAAAT
CTACTACAATTCATCTAGAGCATAATAATTTAGAAGAAATTTCCATTTCTCTTCTCTAAATCT
CTGGAAGACTCCTTCTTGGTTACAATGAAATCTCCAACTGCAGACAAATGCTATGGATGGG
CTAGTAACTTGACCATGCTTGATCTCTGTTATAATTATCTTCATGATTCCTGCTAAAAGAC
AAAATCTTTGCCAAATGGAAAACTAATGCAGCTCAACCTCTGCAGTAACAGATTAGAATCA
ATGCCTCCTGGTTTGCTTCTTCACTTATGTATCTGTCTTTAGAAAATAATTCATTTCTTCT
ATACCCGAAAAATACTTCGACAACTTCCAAAACCTCATACTCTAAGAATGTCACACAACAA
CTACAAGACATCCCATATAATATTTTAATCTTCCCAACATTGTAGAACTCAGTGTGGACAC
AACAAATTGAAGCAAGCATTCTATATTCCAAGAAATTTGGAACACCTATACCTACAAAATAAT
GAAATAGAAAAGATGAATCTTACAGTGATGTGTCCTTCTATTGACCCACTACATTACCACCAT
TTAACATACATTGCTGTGGACCAAAATAAACTAAAAGAACCAATAAGCTCATACATCTTCTTC
TGCTTCCCTCATATACACACTATTTATTATGGTGAACAACGAAGCACTAATGGTCAAACAATA
CAACTAAAGACACAAGTTTTTCAGGAGATTTCAGATGATGATGATGAAAGTGAAGATCAGAT
GATCTGACAATGCTCATGAGAGCCAGAACAAGAAGGAGCAGAAGGGCACTTTGACCTTCAT
TATTATGAAAATCAAGAATTAGCAAGAACTATATAGGTATACACTTACGACTTCACAAAACCTA
TACTTAATATAGTAAATCTAAGTAAACATGTATTACTCAAAGTAATATATTTAGAATTATGTA
TTAGTATAAGATCAGAATTGAATTTAAGTTGTTGGTGACATCTGCATCATTTTCATAGGATTAG
AACTTACTCAAATAATGTAATCTTTAAAAATATAAATTAGAATGACAAGTGGGAATCATAA
ATTAACGTTAATGGTTTCTTATGCTCTTTTAAATATAGAAATATCATGTTAAAGAAAAAA
AAAAAA

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FIGURE 302

MGFLSPIYVIFFFFGVKVHCQYETYQWDEDYDQEPDDDYQTGFPPFRQNVGYGVPPHQYTLGCV
SECFPCPTNFPSSMYCDNRKCLKTIPNIPMHIQQLYLQFNEIEAVTANSFINATHLKEINLSHNK
IKSQKIDYGVFAKLPNLLQLHLEHNNLEEFPPPLPKSLERLLLGYNEISKLQTNAMDGLVNL
MLDLCYNYLHDSLLKDKIFAKMEKLMQLNLCSNRLESMPPGLPSSSLMYLSLENNISSIPEKY
FDKLPKLHTLRMSHNKLQDIPYNIFNLPNIVELSVGHNKLKQAFYIPRNLEHLYLQNNIEKM
NLTVMCPSIDPLHYHHLTYIRVDQNKLEPISSYIFFCFPHIHTIYYGEQRSTNGQTIQLKTQ
VFRFPDDDDDESDHDDPDNAHESPEQEGAEGHFDLHYENQE

Important features:**N-glycosylation sites:**

Amino acids 113-117;121-125; 187-191;242-246;316-320

Tyrosine kinase phosphorylation sites:

Amino acids 268-275;300-307

N-myristoylation site:

Amino acids 230-236

Leucine zipper patterns:

Amino acids 146-168;217-239

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FIGURE 303

GCCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAGC
TGCAGCCTTTTGA AACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTACCA
CGCTTGTTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCACAGCATGAATCTGGT
AGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTTGTTCTTATGAT
ACTGTGCTTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCTCTGGGGGTTT
AAATGTACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCTCCTGAAACAGT
CTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTTAAGGACCTCCA
TCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTGAGTTTATCGATGAGCATGCCTTCAA
AGGAGTAGCTGAAACCTTGCAAGCTCTGGACTTGTCCGACAATCGGATTCAAAGTGTGCACAA
AAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAACCCCTGGCACTGCGACTG
TACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAACGTGATCTG
TAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCTCAATGCTGCCAACGACGCTGA
CCTTTGTAACCTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCATTGTTGGCTGGTT
CACTATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAGGATGCCCGGAGACA
CCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAGAAAGCAGATGAACCTGATGATATTAG
CACTGTGGTATAGTGTCCAAACTGACTGTCAATTGAGAAAGAAAGAAAGTAGTTTGCGATTGCA
GTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAAACATTTGAAACTTTGTATTTCAGTTT
TTTTTGAATTATGCCACTGCTGAACTTTTAAACAACACTACAACATAAATAATTTGAGTTTAG
GTGATCCACCCCTTAATTGTACCCCGATGGTATATTCTGAGTAAGCTACTATCTGAACATT
AGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTTAATTTAAAAGCAAATAAAAG
CTTAACCTTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAAACA

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FIGURE 304

MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMC PKGCLCSSSGGLNVTCSNANLKEI PRDLP
PETVLLYLD SNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDSL DNRIQ
SVHKNAFNNLKARARIANNPWHC DCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPF LNAA
NDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVVYVRQNQEDARRHLEYLKS LPSRQKKADEP
DDISTVV

Important features:**Signal sequence:**

Amino acids 1-33

Transmembrane domain:

Amino acids 204-219

N-glycosylation sites:

Amino acids 47-51;94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation sites:

Amino acids 37-43;45-51;110-116

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FIGURE 305

CGCCACCACCTGCGGCCACCGGCCAATGAAAGCGCTCCGCTCCTAGTGGTTTTTCCACTTTGTTGAATTGTTCTCT
 ATACTCAAAATGTCACCAAGACACCTTGTCTCCCAAATGCAAAATGTGAAATACGCAATGGAAATGAGAGCCTGCT
 ATTCCACATATGGGATTTTCAGGAAATGGGTGCACAATTTGTGAAGATGATCAATGAATGTGGAAATTTAACTCAGT
 CCTGTGCGCAAAATGCTTAATGCACTAACACAGAGGAAGTTATATTGTTATGCTGTGTACCTGGGCTTCAGATCA
 GCAGTAACCAAGACAGGTTTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACTGCCATTTAG
 ATAATGTCTGTATAGCTGCAAAATATTAAATAAACTTTAAACAAAAATCAGATCCATAAAAGAACCTGTGGCTTTGCC
 TACAAAGAGTCTATAGAAAATTCGTGACAGATCTTTCACCAACAGATATAATTACATATATAGAAATATTAGCTGT
 AATCATCTTCATTACTAGGTTTACAAGAACCAACACTATCTCAGCCAAGGACACCCCTTCTAAGCTCAAGCTCTTACGT
 AATTTGTAAAAACCGTGAATAATTTTGTCAAAGGGATACATTTGTAGTTTGGGACAAAGTTATCTGTGAATCATA
 GGAGAACACATCTTACAAAACTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCAGAGCTTCCAAAAGA
 CCACAGAGTTTGATACAAATTCACCGGATATAGCTCTCAAAGTTTCTTTTTTGATTCATATAGCATGAAACATA
 TTTCTCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAAGAGAAAAGCTGCATATGATTCAAATG
 GCAATGTTGCGATTTGCATTTTTATATTATAAGAGTATGGTCCCTTGGCTTTCATCATCTGCAACTCTCTATTGA
 AACCTCAAAATTTTGATAAATTCGAAGAGGAGGAAAGAGTCATATCTCAGTAATTTTCAGTCTCAATGAGCTCAA
 ACCACCACCATTTATATGAAGCTTGA AAAAATAACATTTACATTAAGTTCATCGAAGGTCACAGATAGGTATAGGA
 GTCTATGTGCAITTTTGGAAATTA CTACCTGATACCATGAATGGCAGCTGGTCTTCAGAGGGCTGTGAGCTGACAT
 ACTCAAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACATTTTGCRAATTTTGATGTCTCTGTGCTCTT
 CCATTGGTATTAAAGATTATATATTCTTACAAAGGATCACTCAACTAGGAATTAATTTTCACTGATTTGTCTTG
 CCATATGCATTTTTACCTCTCGGTTCTTCAGTGAATTCAAAGCACCAGGACACAAATTCACAAAAATCTTTGCT
 GTAGCCTATTTCTGTCTGAATTTGTTTTCTTGTGGGATCAATACAAATACTAATAAGCTCTCTGTCTCAATCA
 TTGCCGGACTGCTACACTACTCTTTTTTAGCTGCTTTTGCAATGGATGTGCATTGAAGGCATACATCTCTATCTCA
 TTGTTGTGGGTGTCTATCTACAAACAGGGATTTTGCACAAGAAATTTTATATCTTTGGCTATCTAAGCCAGCGG
 TGGTAGTTGGATTTTCGGCAGCACTAGGATACAGATATTATGGCACAACCAAGATGTTGGCTTAGCACCAGAAA
 ACAACTTTATTTGGAGTTTATATAGGACCAGCATGCCATATCTTCTGTTAATCTCTGGCTTTGGAGTCATCA
 TATACCAAAATTTTCGTCCACACTGCAGGGTTGAAACCAAGAGTTAGTTGCTTTGAGAACATAGGCTCTTGTGCAA
 GAGGAGCCCTCGCTCTTCTGTCTCTCTCGGCACACCTGGATCTTTGGGGTTCTCCATGTTGTGCGAGCATCAG
 TGGTTACAGCTTACCTCTTCACAGTCAGCAATGCTTTCCAGGGGATGTTCAATTTTTTATTCCTGTGTGTTTTAT
 CTAGAAAGATTCAAGAAGAAATATTACAGATTGTTCAAAATGTCCCCTGTGTTTTGGGATGTTAAAGGTAACAT
 AGAGAAATGGTGGATAATTACAACTGCACAAAAATAAAATTTCCAGCTGTGGATGACCAATGTATAAAAATGACT
 CATCAAAATATCCAAATTTATTAAC TACTAGACAAAAAGTATTTAAATCAGTTTTTCTGTTTATGCTATAGGAAT
 GTAGATAATAAGGTAAAAATATGTATCATATAGATATACTATGTTTTCTATGTGAAATAGTTCTGTCAAATA
 GTATTGCAGATATTTGGAAAGTAAATTTGGTTTCTCAGGAGTGATATCACTGCACCAAGGAAAGATTTTCTTTCTA
 ACACGAGAGATATATGAATGTCTGGAAGGAAACCACTGGCTGATATTTCTGTGACTCGTGTTGCTTTGAAACT
 AGTCCCCACCACTTCGGTAATGAGCTCCATTACAGAAAGTGAACATAGAGAAATGAAGGGGCAGAAATATCAAA
 CAGTGAAGAGGGAATGATAAGTGTATTTTGAATGAAGTGTTTTTCTGTAGACTAGCTGAGAAATGTTGTGACAT
 AAAATAAGAAATGAAGAAACATGTTTTACCAATTTTGTGAATTTGTCAGACTTAAATGTCATCAAAACAACTT
 AGACTCTGTTTTGCTAAATCTGTTTTCTTTTCTAATATTCAAAAAAAAAGAGGTTTACTCTCCACAAATTTGA
 AA

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FIGURE 306

MKRLPLLVLVVFSTLLNCSYTONCTKTCLPLNAKCEIRNGIEACYCNMGFSGNGVTICEDDNECGNLTQSCGENANC
TNTGSSYYCMCVPGFRSSSNQDRFITNDGTVCIENVNANCHLDNVCIANINKTLTKIRSIKEPVALLQEVYRNS
VTDLSPTDIIITYIEILAESSLLGYKNNTISAKDTLSNSTLTFVKTVNNFVQDRDFVVDKLSVNHRRTHLTKL
MHTVEQATLRISQSFQKTTEFDTNSTDIALKVFFFDSDYNMKHIHPHMNDGDYINIFFPKRKAAYDSNGNVAVAF
YYKSIGPLSSSDNLFLLKPQYNDSEEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDYRSLCAFWNY
SPDTMNGSWSSGECELTYSNETHSCRCNHLTHFAILMSSGPGSIGIKDYNILTRITQLGIIISLICLAICIFTFW
FFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSTIAGLLHYFFLAFAWMCIEGTHLYLIVVGVYN
KGFLHKNFYIFGYLSPAVVVGFSAAALGYRYGTTKVCWLSTENNFWSFIGPACLIILVNLLAFGVIIYKVFRT
AGLKPEVSCFENIRSCARGALALLFLLGTTWIFGVLVHVVHSAVVTAYLFTVSNAFQGMFIPLFLCVLSRKTIQEEY
YRLFKNVPCCFGCLR

Important features:**Signal peptide:**

Amino acids 1-19

Transmembrane domain:

Amino acids 431-450;494-515;573-594;619-636;646-664

N-glycosylation sites:

Amino acids 15-19;21-25;64-68;74-78;127-131;177-181;

188-192;249-253;381-385;395-399

Glycosaminoglycan attachment site:

Amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 360-364

Tyrosine kinase phosphorylation sites:

Amino acids 36-44;670-677

N-myristoylation sites:

Amino acids 38-44;50-56;52-58;80-86;382-388;388-394;

434-440;480-486;521-527

Aspartic acid and asparagine hydroxylation site:

Amino acids 75-87

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FIGURE 307

CCAGGCCGGGAGGCGACGCGCCAGCCGCTCTAAACGGGAACAGCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGT
ATCTGACGCGCGCCAGGTTGCGTAGGTGCGGCACGAGGAGTTTTCCCGCGACGAGGAGGTCCTGAGCAGCA**ATGGC**
CCGGAGGAGCGCCTTCCCTGCCGCCGCGCTCTGGCTCTGGAGCATCCCTCCTGTGCTGCTGGCACTGCGGGCGGA
GGCCGGGCGCGCGCAGGAGGAGAGCCCTGTACTATGGATCGATGCTCACCAGGCAAGAGTACTCATAGGATTTGA
AGAAGATATCCTGATTGTTTCAGAGGGGAAAATGGCACCTTTTACACATGATTTTCAGAAAAGCGCAACAGAGAAT
GCCAGCTATTCTCTGCAATATCCATTCCATGAATTTTACCTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGA
ATTCTCTGTCCCTGCCCTCCCTGGATAAAGGCGATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGT
GCCCTCACAGGCGATCAGTTGTTCAAGTTGGTTTCCCATGTCTTGGAAAAACAGGATGGGTGGCAGCATTTGAAGT
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTCAAATGCTATCTTCTTTAAACATG
TCAACAAGCTGAGTGCCACGGCGGGTGCCGAAATGGAGGCTTTTGTAAATGAAAGACGCATCTGCGAGTGTCCCTGA
TGGGTTCACGGACCTCACTGTGAGAAAGCCCTTTGTACCCACGATGTATGAATGGTGGACTTTGTGTGACTCC
TGGTTTCTGCATCTGCCACCTGGATTCTATGGAGTGAAGTGTGACAAAGCAAATGCTCAACCACTGCTTTAA
TGGAGGGACCTGTTTCTACCTCGGAAATGTATTGGCCTCCAGGACTAGAGGGAGAGCAGTGTGAATCAGCAA
ATGCCCAACCCCTGTGCAATGGAGGTAAATGCATTGGTAAAGCAAATGTAAGTGTCCAAAGGTTACCAGGG
AGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGCACATGGAACCTGCCATGAACCCAACAATGCCA
ATGTCAAGAAGGTTGGCATGGAAGACACTGCAATAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGC
AGCGGCCAGCTCAGGCAGCACAGCCTTCACTTAAAGCCGAGGAGCGCGGGATCCAGCTGAATCCAATTA
CATCTGCT**GGA**ACTCCGACATCTGAAACGTTTTAAGTTACACCAAGTTCAATAGCCTTTGTAAACCTTTCATGTGTT
GAATGTTCAAATAATGTTTCACTTAAGAATACTGGCCTGAATTTTATTAGCTTCATTATAAATCACTGAGC
TGATATTTACTCTTCCCTTTAAGTTTCTAAGTACGCTCTGTAGCATGATGGTATAGATTTTCTTGTTCAGTGCT
TTGGGACAGATTTTATATATGTCAATTTGATCAGGTTAAATTTTCACTGTGTAGTTGGCAGATATTTCAAAT
TACAATGCATTTATGGTGTCTGGGGCAGGGGAACATCAGAAAGGTTAAATTTGGGCAAAATGCGTAAATCACAA
GAAATTTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTTCAATTTTATTGTCAGATATTTAGATGTTGTTTAC
ATTTTAAAAAATGCTCTTAATTTTAAACTCTCAATACAAATATATTTTGACCTTACCATTATTTCCAGAGATTCA
GTATTAATAAAAAAAAAATTAACCTGTGGTAGTGGCATTAAACAAATATATATATTTCTAAACAAATGAAATAG
GGAATATAATGATGAACCTTTTGCATTGGCTTGAAGCAATATAATATATTGTAAACAAAAACAGCTCTTACCT
AATAAACATTTTATAGCTTGTGTATGTATAAAATAAAGGTGCTGCTTTTAGTTTTTGGAAAAAATAAAAAAAAA
AAAAAAA

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FIGURE 308

MARRSAFPAAALWLSILLCLLALRAEAGPPQEEESLYLWIDAHQARVLIGFEEDILIVSEGKM
APFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPLGT
VPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNLILQTPQNAIFFKTCQQAECPPGGCRNG
GFCNERRICECPDGFHGPHEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCSTTCFN
GGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKCSKGYQGDLCSPVCEPGCG
AHGTCHEPNKQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDPPESNYIW

Important features:**Signal sequence:**

Amino acids 1-28

N-glycosylation sites:

Amino acids 88-92;245-249

Tyrosine kinase phosphorylation site:

Amino acids 370-378

N-myristoylation sites:

Amino acids 184-190;185-191;189-195;315-321

ATP/GTP-binding site motif A (P-loop):

Amino acids 285-293

EGF-like domain cysteine pattern signatures:

Amino acids 198-210;230-242;262-274;294-306;326-338

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FIGURE 309

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTCGCGCACAGATGCGGG
TTAGACTGGCGGGGGAGGAGGCCGAGGAGGGAAGGAAAGCTGCATGCATGAGACCCACAGACT
CTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGATCATGGAATGAACCCGAGCAATGGAG
ATGGATTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTGCCCG
TGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTTTCGATG
ACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCGAGGGAGGGG
TTTTCTTTGAAGGCTCTGTAGCCGATTTCAGTGCACAGACGGATTCAAGCTGAAGGGCGCTA
CAAAGAGACTGTGTTGAAGCATTTTAAATGGAACCTAGGCTGGATCCCAGTGATAATTCCA
TCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCTATAACAAGACAT
ATAGACATGGAGAGAAGCTAATCATCACTTGTGATGAAGGATTCAAGATCCGGTACCCCGACC
TACACAATATGGTTTCATTATGTGCGGATGATGGAACGTGGAATAATCTGCCCATCTGTCAAG
GCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAACATCTCTGAGCTCCAGACCTCCT
TCCCGTGGGGACTGTGATCTCCTATCGCTGCTTTCCCGGATTAAACTTGATGGGTCTGCGT
ATCTTGAGTGCTTACAAAACCTTATCTGGTGTGTCAGGCCACCCCGGTGCGTTGCTCTGGAAG
CCCAAGTCTGTCCACTACCTCCAATGGTGAGTACGGAGATTTCGTCTGCCACCCGCGGCCCTT
GTGAGCGCTACAACCACGGAAGTGTGGTGGAGTTTACTGCGATCCTGGCTACAGCCTCACC
GCGACTACAAGTACATCACTGCCAGTATGGAGAGTGGTTTCCTTCTTATCAAGTCTACTGCA
TCAAATCAGAGCAACCGTGGCCAGCACCCATGAGACCTCCTGACCACGTGGAAGATTGTGG
CGTTCACGGCAACCAAGTGTGCTGCTGGTGTGCTGCTCATCTGCGCAGGATGTTCCAGA
CCAAGTTCAGGCCCCACTTTCCCCCAGGGGGCTCCCGGAGTTCAGCAGTGACCTGACT
TTGTGGTGTGAGACGGCGTCCCCGTGCTGCTCCCGTCTATGACGAAGCTGFGAGTGGCGGCT
TGAGTGCTTAGGCCCCGGGTACATGGCCTCTGTGGGCCAGGGCTGCCCCCTACCCGTGGACG
ACCAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGACACAGGGCCAGGGGAGTCAGAAA
CCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAAGTCTGTATTACCTCCAGGTGCC
AAGAGAGCACCACCCCTGCTTCGGACAACCTGACATAATTGCCAGCAGCGCAGAGGAGGTGG
CATCCACCAGCCCCAGGCATCCATCATGCCCACTGGGTGTTGTTCTTAAGAAACATGATTGATTA
AAAAATTTCCCAAAGTGTCTGAAGTGTCTCTTCAAATACATGTTGATCTGTGGAGTGTGATTC
CTTTCCTCTCTTGGTTTGTAGACAAATGTAACAAAGCTCTGATCCTTAAATTTGCTATGCTG
ATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTCTGTTTCTTCTTACACAGACTGATTAA
AATTAAGNAAAAA

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FIGURE 310

MYHGMNPSNGDGFLEQQQQQQPQSPQRLLAVILWFQLALCFGAQLTGGFDDLQVCADPGIP
ENGFRTPSGGVFFEGSVARFHCQDGFKLKGTKRLCLKHFNGTLGWIPSPDNSICVQEDCRIPQ
IEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLASSNG
YVNISELQTSFFVGTVISYRCFPFGKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLPPMVS
HGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQTWPSTH
ETLLTTWKIVAFTATSVLLVLLLVILARMFQTKFKAHFPPRGPFRSSSSDPDFVVVDGVPVML
PSYDEAVSGGLSALGPGYMASVGQCPLPVDQSPFAYPGSGDPTDTPGGESETCDSVSGSSEL
LQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWLFLRN

Important features:**Signal sequence:**

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472**N-myristoylation site.**amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405

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FIGURE 311

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGAG
CGTGGCGAACAGGGGCTCTGGGGCTGGCGCTGCTGCTGCTCGGCTCGGACTAGGCCTGG
AGGCCGCGCGAGGCCCGCTTTCCACCCCGACCTCTGCCAGGCCGAGGCCCCAGCTCAGGCT
CGTGGCCACCCACCAAGTTCCAGTGCCGACCCAGTGGCTTATGCGTGCCCCCTCACCTGGCGCT
GCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCCATGTA
CCCAGAAAGGGCAATGCCACCGCCCCCTGGGCTCCCCTGCCCTGCACGGCGTCAGTGACT
GCTCTGGGGAACTGACAAGAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCAGGCGAGC
TCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCACCCAGACT
GTCCCAGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGAAGGGGATGCCA
CAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTACCTCTCTCAGGAATGCCACAACCATGG
GGCCCCCTGTGACCCTGGAGAGTGTCCCCTCTGTGCGGAATGCCACATCCTCCTCTGCCGGAG
ACCAGTCTGGAAGCCCAACTGCCTATGGGGTTATTGCAGCTGCTGCGGTGCTCAGTGCAAGCC
TGGTCACCGCCACCCTCCTCCTTTTGTCTGGCTCCGAGCCCAGGAGCGCTCCGCCCCACTGG
GGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTGAGAACAAGAAGACCTCGCTGCCCTTGAG
GACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACAGGAGGAGAGCAGTGA
TGCGGATGGGTACCGGGGCACACCAGCCCTCAGAGACCTGAGTTCCTCTGCCCACGTGGAACC
TCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCCTGGACACTCCCTATGGA
GATCCGGGGAGCTAGGATGGGGAACCTGCCACAGCCAGAAGTGAAGGGCTGGCCCCAGGCAGC
TCCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTGCCCCGCTGAGGGTGGCGA
TTAAAGTTGCTTC

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FIGURE 312

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPTKFCQRT
SGLCVPLTWRCDRDLDCSDGSDEEECRIEPTQKGQCPPPPGLPCPCTGVSDCSGGTDKKLRN
CSRLACLAGELRCTLSDDCIPLTWRCDHDPDCPDSSDELGCGTNEILPEGDATTMGPPVTLES
VTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAVLSASLVTTATLLLSW
LRAQERLRPLGLLVAMKESLLLSEQKTSLP

Important features:**Signal sequence:**

Amino acids 1-30

Transmembrane domain:

Amino acids 231-248

N-glycosylation sites:

Amino acids 126-130;195-199;213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation sites:Amino acids 3-9;10-16;26-32;30-36;112-118;166-172;212-218;
224-230;230-236;263-269**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 44-55

Leucine zipper pattern:

Amino acids 17-39

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FIGURE 313

CGGACGCGTGGGCGTCCGGCGGTGCGAGAGCCAGGAGGCGGAGGCGCGCGGGCCAGCCTGGGCCCCAGCCACAC
CTTCACCAGGGCCCCAGGAGCCACCATGTGGCGATGTCCACTGGGGCTACTGCTGTTGCTGCGCGTGGCTGGCCAC
TTGGCTCTGGGTGCCACGAGGGTCCGTGGCGCGGGAGCTAGCACCGGGCTCTGCACCTGCGGGGCATCCGGGAC
GCGGGAGGGCCGGTACTGCCAGGAGCAGGACCTGTGCTGCGCGGGCTGTGCCGACGACTGTGCCCTGCGCTACCTG
GGCGCCATCTGTTACTGTGACCTCTTCTGCAACCGCAGCGTCTCCGACTGCTGCCCTGACTTCTGGGACTTCTGC
CTCGGCGTGCCACCCCTTTTCCCCCGATCCAGGATGTATGCATGGAGGTCGTATCTATCCAGTCTTGGGAACG
TACTGGGACAACTGTAAACGTTGCACTGCCAGGAGAACAGGCAGTGGCATGTGGATCCAGACATGATCAAAGC
CATCAACAGGGCAACTATGGCTGGCAGGCTGGGAACCAGCGCCTTCTGGGGCATGACCCTGGATGAGGGCAT
TCGCTACCGCTGCGGCACCATCCGCCATCTTCTTCGGTTCATGAACATGCATGAAATTTATACAGTGTGAACCC
AGGGGAGGTGCTTCCACAGCCTTCGAGGCTCTGAGAAGTGGCCCAACCTGATTCATGAGCCTCTTGACCAAGG
CAACTGTGCAGGCTCCTGGGCCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCATCAATCCATTCTCTGGGACA
CATGACGCTGTCCCTGTGCGCCCCAGAACCTGCTGTCTTGACACCCACAGCAGCAGGGCTGCCGCGGTGGCG
TCTCGATGGTGCTGCTGGTTCCTGCGTCGCCAGGGGTGGTGTGTGACCACTGCTACCCCTTCTCGGGCGTGA
ACGAGACGAGGCTGGCCCTGCGCCCCCTGTATGATGCACAGCCGAGCATGGGTGCGGGCAAGCGCCAGGCCAC
TGCCCACTGCCCCAACAGCTATGTTAATAACAATGACATCTACAGGTCACTCCTGTCTACCGCCTCGGCTCCAA
CGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGGTGCATGAGGACTTCTT
CCTATACAAGGAGGCTATCTACAGCCACACGCCAGTGAAGCTTGGGAGGCCAGAGAGATACGCCCGGCATGGGAC
CCACTCAGTCAAGATCACAGGATGGGGAGGAGGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGC
CAACTCCTGGGGCCAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGCGCGGCGTCAATGAGTGCACATCGA
GAGCTTCGTGCTGGGCGTCTGGGGCCGCGTGGGCATGGAGGACATGGGTCACTACTGAGGCTGCGGGCACCACGC
GGGGTCCGGCTGGGATCCAGGCTAAGGGCCGCGCGAAGAGGCCCAATGGGGCGGTGACCCAGCCTCGCCCGA
CAGAGCCCGGGCGCAGGCGGGCGCCAGGGCGCTAATCCGGCGCGGGTTCGCTGACGCAGCGCCCCCGCTGGG
AGCGCGGGCAGGCGAGACTGGCGGAGCCCCAGACCTCCGACTGGGACGGGCGAGGCTGGCTGGGAAGAG
CACAGCTGCAGATGCCAGGCTCTGGCGCCCCACTCAAGACTACCAAGCCAGGACACCTCAAGTCTCCAGCCC
CAATACCCACCCCAATCCGCTATTCTTTTTTTTTTTTTTTAGACAGGGTCTGCTCCGTGCCCAGGTTGGAG
TGCAGTGGCCCATCAGGGCTCACTGTAACTCCGACTCCGGTTCAAGTGACCTCCCACTCAGCCTCTCAAG
TAGCTGGGACTACAGGTGCACACCCACCTGGCTAATTTTGTATTTTTTTGTAAGAGGGGGGTCTCACTGTGT
TGCCAGGCTGGTTTCGAACCTCTGGGGTCAAGCGGTCCACCTGCCTCCGCTCCCAAAGTGCTGGGATTCAGG
CATGAGCCACTGCACCCAGCCCTGTATTCTTATCTTCAGATATTAATTTTCTTTTCACTGTTTTAAATAA
CCAAAGTATTGATAAAAAAAA

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FIGURE 314

MWRCPLGLLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADDDCA
LPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPFPPIQGCMHGGRIYPVLGTYWDCNRCT
CQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

Important features:**N-glycosylation site.**

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

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FIGURE 315

CGGACGCGTGGGCCCTGGTGGGCCAGCAAGATGGATCTACTGTGGATCCTGCCCTCCCTGT
GGCTTCTCCTGCTTGGGGGGCCTGCCCTGCCCTGAAGACCCAGGAACACCCAGCTGCCAGGAC
CCAGGGAAC TGGAAGCCAGCAAAGTTGTCTCCTGCCAGTTGTCCCGAGCTCCAGGAAGTC
CTGGGGAGAAGGGAGCCCCAGGTCCTCAAGGGCCACCTGGACCACCAGGCAAGATGGCCCCA
AGGGTGAGCCAGGCCCCAGAACTGCCGGGAGCTGTTGAGCCAGGGCGCACCTTGAGCGGCT
GGTACCATCTGTGCCTACCTGAGGGCAGGGCCCTCCAGTCTTTTGTGACATGGACACCGAGG
GGGGCGGCTGGCTGGTGTTCAGAGGCGCCAGGATGGTTCTGTGGATTCTTCCGCTCTTGGT
CCTCCTACAGAGCAGGTTTTGGGAACCAAGAGTCTGAATTCTGGCTGGGAAATGAGAATTTGC
ACCAGCTTACTCTCCAGGTAAC TGGAGCTGCGGGTAGAGCTGGAAGACTTTAATGGTAACC
GTACTTTGCGCCACTATGCGACCTTCGCGCTCCTCGGTGAGGTAGACCCTACCAGCTGGCAC
TGGGCAAGTTCTCAGAGGGCACTGCAGGGGATTCCCTGAGCCTCCACAGTGGGAGGCCCTTTA
CCACCTATGACGCTGACCACGATTCAAGCAACAGCAACTGTGCAGTGATTGTCCACGGTGCCCT
GGTGGTATGCATCCTGTTACCGATCAAATCTCAATGGTCGCTATGCAGTGCTGAGGCTGCCG
CCCACAAATATGGCATTGACTGGGCCTCAGGCCGTGGTGTGGGCCACCCCTACCGCAGGGTTC
GGATGATGCTTCGATAGGGCACTCTGGCAGCCAGTGCCTTATCTCTCCTGTACAGCTTCCGG
ATCGTCAGCCACCTTGCCCTTTGCCAACCACCTCTGCTTGCCTGTCCACATTTAAAAATAAAAT
CATTTTAGCCCTTTC A

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FIGURE 316

MDLLWILPSLWLLLLGGPACLKQTQEHFSCPGPRELEASKVVLLFSCPGAPGSPGEKGAPGPQG
PPGPPGKMGPKGEPGPRNCRELLSQGATLSGWYHLCLPEGRALPVFCDMDTEGGGWLVFQRRQ
DGSVDFFRSWSSYRAGFGNQESEFWLGNENLHQLTLQGNWELRVELEDFNGNRTFAHYATFRL
LGEVDHYQLALGKFSEGTAGDSLHSGRPFTTYDADHDSSNSNCAVIVHGAWWYASCYRSNL
NGRYAVSEAAAHKYIDWASGRGVGHPYRRVRMLR

Important features:**Signal peptide:**

Amino acids 1-16

N-glycosylation site:

Amino acids 178-182

Glycosaminoglycan attachment site:

Amino acids 272-276

Tyrosine kinase phosphorylation site:

Amino acids 188-197

N-myristoylation sites:

Amino acids 16-22;89-95;144-150;267-273

Fibrinogen beta and gamma chains C-terminal domain signature:

Amino acids 242-255

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FIGURE 317

CCCAAGCCAGCCGAGCCGCCAGAGCCGCGGGCGCGGGGTGTTCGCGGGGCCCAACCCAGGAT
GCTCCCTCGGCGCTCTGCTCTACCGGCTCTCTACTGCTCTGGCGGCTGTCTACTTGTCTT
GGGATCAGGTTCTCTCTCAGGATTTCTGAAGCGCCGACAGCTACACGGAATGCACAGATGGCTA
TGAGTGGGACCCAGACAGCCAGCACTGCGGGGATGTCAACAGAGTGTCTGACCATCCCTGAGGC
CTCGAAGGGGGAAATGAAGTGCATCAACCACTACCGGGGCTACTTGTGCTTCCCGCTCCGCTCCG
TGCGCTCATCAACCACTACATGCGGAGGAGCCCGCGACCAAGTGCTCTCCGCTCAACACC
TAACCCCTGCCCAACAGGCTATGAGCCCGACGATCAGGACAGCTGTGTGGATGTGGACGAGTG
TGCCCGAGGCGCTGCACAGCTGTGCCCGCAGCCAGGACGCGATGCCTAACTTGCTTGGCTGCTATCA
GTGCACCTGCCCTGATGGTTACCGCAAGATCGGGCCGAGTGTGTGGACATAGACAGAGTGC
CTACCGCTACTGCCAGCACCGCTGCGTGAACCTGCTTGGCTCTTCCGCTGCCAGTGCAGGC
GGGCTTCAGCTGTGGGCGCTAACACCGCTCTGTGTGATGTGACGAGTGTGCATAGGGGGC
CCCATCGAGCAGCGCTGCTTCAACTCTATGGACACTTCTGTGTGCTGCCACAGGCTA
TGAGCTGCATCGGGATGGCTTCTCTGCAAGTGATATTGATGAGTGTAGCTACTCCAGCTACCT
CTGTGAGTACCGCTGCGCTACAGCAGCGAGCGGCTTGTCTCTGCCACTGCCACAGGTTACCA
GCTGCTGGCCACAGCCTGTGCCAAGACATTAGTAGTGAGTGTCTGTGTGGCAGCAAGTGTCT
CGAGGCCCAAACCTGTGTCAACTTCCATGGGGCTACCGCTGCGTGGACACCAACCGCTGCGT
GGAGCCGTACATCTCAGGCTCTGTGAGAACCGCTGTGCTTGGCCGGCGCTCAACCGCTATGTGCG
AGAGCAGCCTTCATCTATTGTGACCGCTACATGACCATCACTCGGAGCGAGCGTGGCCCG
TGACGTGTTCCAGATCCAGGCGACCTCCGCTTACCCCGGTGCCCTACAATGCCTTTCAGATCCG
TCTGTGAAACTCGCAGGGGAGCTTTACATTAGGCAATCAACACAGTCAAGCGCATGCTGGT
CCTCGCCCGCGCGGTGACGGCGCCCGGGAGTACGTCTGGACCTGGAGATGCTCAACCTGAA
TTCCCTCATGAGCTACCGGCGACGCTGTACTGAGGCTACCGCTCTTTGTAGGGCGCTACAC
CTTCTGAGAGAGCAGGAGGGAGCCACCTCTCTGAGCTACCTTAGCTGAGGAGCGCTGTTGTGA
GGGCGAGATGAGAAGGCCAATAAAGGAGAAGAAGTCTGTGTGCTGAGGTGGCGGGCT
ACACTGCAGGAAGCCTCAGGCTGGGGCAGGGTGGCACTTGGGGGGGCGAGGCCAAGTTCACCTA
AATGGGGTCTCTATATGTGAGGCTCAGGCGCGCCCACTGACAGGAGCTGGGAGCTCTGCAC
CAGAGATTTCACTGACCCCGAGGAGGAGGAGTACAGGAGGCGGCACTCAGGCCCGCG
CCAGAGATTTGGAAGTGGCTGGCTTGCAGGGGTCCTAAGAAACTGCACTCTGGACAGCGCCAG
GAGGCCCGTGGGTTCATCTCAACTCTGCTCAAACTGGATTTGGATAAGCCCTTAGTAGT
CCCTGGGCGCTGTTTTCTATAAAACGAGGCACTGAAAAAAAAAAAA

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FIGURE 318

MLPCASCLPGSLLLWALLLLLLLGSASPQDSEEPDSYTECTDGYEWDPPDSQHCRD VNECLTIPE
ACKGEMK C I N H Y G G Y L C L P R S A A V I N D L H G E G P P P P V P P A Q H P N F C P P G Y E P D D Q D S C V D V D E
CAQALHDCRPSQDCHNLPGSYQCTCPDGYRKIGPECVDIDECYRYCQHRCVNLPGSFRCQCE
PGFQLGPNNRSCVDVNECDMGAPCEQRCFNSYGTFLCRCHQGYELHRDGFSCSDIDEC SYSSY
LCQYRCVNEPGRFSCHPQGYQLLATRLCQDIDECESGAHQCSQAQTCVNFHGGYRCVDTNRC
VEPYIQVSENRLCPASNPLCREQPSSI V H R Y M T I T S E R S V P A D V F Q I Q A T S V Y P G A Y N A F Q I
RAGNSQGDFYIRQINNVSAMLVLARFVTGPREYVLDLEMVTMNSLMSYRASSVLRLTVFVGAYTF

Important features:**Signal sequence:**

Amino acids 1-25

N-glycosylation sites:

Amino acids 198-202;394-398

N-myristoylation sites:Amino acids 76-82;145-151;182-188;222-228;290-296;305-311;
371-377;381-387**Aspartic acid and asparagine hydroxylation sites:**

amino acids 140-152;177-189;217-229;258-270

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FIGURE 319

GCTGGGGACATGAGAGGCACACCGAAGACCCACCTCCTGGCCTTCTCCCTCCTCTGCCTCCTC
TCAAAGGTGCGTACCCAGCTGTGCCCGACACCATGTACCTGCCCTGGCCACCTCCCCGATGC
CCGCTGGGAGTACCCCTGGTGTGGATGGCTGTGGCTGCTGCCGGGTATGTGCACGGCGGCTG
GGGGAGCCCTGCGACCAACTCCACGTCTGCGACGCCAGCCAGGGCCTGGTCTGCCAGCCCGGG
GCAGGACCCGGTGCCGGGGGGCCCTGTGCCTCTTTGGCAGAGGACGACAGCAGCTGTGAGGTG
AACGGCCGCTGTATCGGAAGGGGAGACCTTCCAGCCCCACTGCAGCATCCGCTGCCGCTGC
GAGGACGGCGGCTTCACCTGCGTGCCGCTGTGCAGCGAGGATGTGCGGCTGCCAGCTGGGAC
TGCCCCACCCCAGGAGGGTCGAGGTCTTGGGCAAGTGCTGCCCTGAGTGGGTGTGCGGCCAA
GGAGGGGGACTGGGGACCCAGCCCTTCCAGCCCCAAGGACCCAGTTTCTGGCCTTGTCTCT
TCCCTGCCCTTGGTGTCCCTGCCCCAGAATGGAGCACGGCCTGGGGACCTGCTCGACCACC
TGTGGGCTGGGCATGGCCACCCGGGTGTCCAACCAGAACCGCTTCTGCCGACTGGAGACCAG
CGCCGCTGTGCCTGTCCAGGCCCTGCCACCCCTCAGGGGTCGAGTCCACAAAACAGTGCC
TTCTAGAGCCGGGCTGGGAATGGGGACACGGTGTCCACCATCCCCAGCTGGTGGCCCTGTGCC
TGGGCCCTGGGCTGATGGAAGATGGTCCGTGCCAGGCCCTTGGCTGCAGGCAACACTTTAGC
TTGGGTCCACCATGCAGAACACCAATATTAAACAGCTGCCTGGTCTGTCTGGATCCCGAGGTA
TGGCAGAGGTGCAAGACCTAGTCCCCCTTCTCTAACTCACTGCCTAGGAGGCTGGCCAAGGT
GTCCAGGGTCTCTAGCCCACTCCCTGCCTACACACACAGCCTATATCAAACATGCACACGGG
CGAGCTTTCTCTCCGACTTCCCTGGGCAAGAGATGGGACAAGCAGTCCCTTAATATTGAGGC
TGCAGCAGGTGCTGGGCTGGACTGGCCATTTTCTGGGGGTAGGATGAAGAGAAGGCACACAG
AGATTCTGGATCTCCTGTGCCTTTTCTGGAGTTGTGAAAAATTGTTCTGAATACAAGCCTAT
GCGTGA

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FIGURE 320

MRGTPKTHLLAFSLCLLSKVRTQLCPTPCTCPWPPPRCPGLGVPLVLDGCGCCRVCAARRLGEP
CDQLHVCDASQGLVCQPGAGPGGRGALCLLAEDDSSCEVNGRLYREGETFQPHCSIRCRCEGDG
GFTCVPLCSEDVRLPSWDCPHPRRVEVLGKCCPEWVGQGGGLGTQPLPAQGPQFSGLVSSLP
PGVPCPEWSTAWGPCSTTCGLMATRVSNQNRFCRLETQRRLLCLSRPCPPSRGRSPQNSAF

Important features:

Signal sequence:

Amino acids 1-23

N-myristoylation sites:

Amino acids 3-9;49-55;81-87;85-91;126-132;164-170;166-172;
167-173;183-189;209-215

Insulin-like growth factor binding proteins signature:

Amino acids 49-65

von Willebrand C1 domain:

Amino acids 107-124

Thrombospondin 1 Homology Block:

Amino acids 201-216

IGF binding protein site:

Amino acids 49-58

FIGURE 321

[illegible]

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FIGURE 322

MMGLSLASAVLLASLLSLHLGTATRGSDISKTCFQYSHKPLPWTWVRSYEFTSNSCSQRAVI
FTTKRGKKVCTHPRKKWVQKYISLLKTPKQL

Important features:**Signal peptide:**

amino acids 1-23

N-myristoylation sites.

amino acids 3-9, 26-32

Amidation site.

amino acids 68-72

Small cytokines (intecrine/chemokine).

amino acids 23-88

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FIGURE 323

ACCGAGCCGAGCGGACCGAAGGCGCGCCGAGATGCAAGGTGAGCAAGAGGATGCTGGCGGGGGCGTGAGGAGCA
TGCCACAGCCCTCTTGGCTGCTGGCAGCCCATCTCTCTGCTGGTGTGGGCTCAGTGCTGTCAGGCTCGGCCA
CGGCTGCCGCCCGCTGCCAGTGCTCCGCCAGGACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAG
TCCCCGAGGGCATCCCCACCGAGACGCGCTGCTGGACCTAGGCAAGAACCGCATCAAAACGCTCAACCAGGACG
AGTTCGCCGAGCTTCCCGACCTGGAGGAGCTGGAGCTCAACGAGAACATCTGTAGCGCCGTGGAGCCCGGCCCT
TCAACAACCTCTTCAACCTCCGACGCTGGGTCTCCGACGCAACCGCTGAAGCTCATCCCGCTAGCGCTCTCA
CTGGCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAGATCGTTATCTCTACTGGACTACATGTTTCAGG
ACCTGTACAACCTCAAGTCACTGGAGGTTGGCGACAATGACCTCTGTCTACATCTCTCACCGCGCTTCAGCGGCC
TCAACAGCCTGGAGCAGCTGACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCACCTGC
ACGGCTCATCTCTGAGGCTCCGGCAGCTCAACATCAATGCCATCCGGGACTACTCTTCAAGAGGCTGTACC
GACTCAAGGTCTTGGAGATCTCCACTGGCCCTACTTGGACACCATGACACCAACTGCCTCTACGGCTCAACC
TGACGTCCCTGTGTCATCACACATGCAATCTGACCGCTGTGCCCTACCTGGCGCTCCGCCACCTAGTCTATCTCC
GCTTCCTCAACCTCTCTCAACCCCATCAGCACCATGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGG
AGATCCAGCTGTGGGGGGGAGCTGGCCGTGGTGGAGCCCTATGCCTTCGGCGGCTCAACTACCTGCGCGTGC
TCAATGTCTCTGGCAACAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGGAGACACTCA
TCTGGACTCCAAACCGCTGGCTGCGACTGTCGGCTCTGTGGGTGTTCCGGCGCCGCTGGCGGCTCAACTTCA
ACGGCAGCAGCCACGCTGCCACGCGCGAGTTTGTCCAGGGCAAGGAGTCAAGGACTTCCCTGATGTGCTAC
TGCCCAACTACTTCACTGCCGCCGCGCCGCATCCGGACCGCAAGGCCAGCAGGTGTTGTGGACGAGGGCC
ACACGGTGCAGTTTGTGTGCCGGGCGGATGGCGACCGCGCGCCGCATCTCTGGCTCTCACCCCGAAAGCAC
TGGTCTCAGCCAAGAGCAATGGCGGCTCACAGTCTTCCCTGATGGCAGCTGGAGGTGCGCTACGCCAGGTAC
AGGACAACGGCAGCTACCTGTGCATCGCGGCCAACGGGGGGGCAACGACTCCATGCCCGCCACCTGCATGTGC
GCAGCTACTCGCCGACTGGCCCCATCAGCCCAACAAGACCTTCGCTTTCATCTCCAACAGCGGGGCGAGGGAG
AGGCCAACAGCACCGCGCCACTGTGCCCTTCCCTTTCGACATCAAGACCTCATCATCGCCACCACCATGGGCT
TCATCTCTTCTCGGGCTGCTCTCTCTCTGCTGGTGTGCTGTTCTTCTGGAGCCGGGGCAAGGGCAACACAA
AGCACAACTCGAGATCGAGTATGTGCCCGAAAGTCGGACGAGGCATCAGTCCGCCGACGCGCCCGCAAGT
TCAACATGAAGATGATATGAGGCGGGGGGGGGGCGAGGACCCCGGGCGGGCGGGCAGGGGAAGGGGCTGGT
CGCCACCTGCTCACTCTCCAGTCTTCCACCTCTCTCTTACCTTCTACACAGCTTCTCTTCTCTCTCTCCGCC
TCCGTCCCCTGCTGCCCCCGCCAGCCCTCACCACTTGCCTTCTTACAGGACCTCAGAAGCCGAGACCTGG
GGACCCACCTACAGGGGCACTGACAGACTGGAGTTGAAGCCGACGAACCGACACGCGGAGAGTCAATAAT
TCAATAAAAAAGTTACGAACCTTCTCTGTAACCTTGGGTTTCAATAATATGAGATTTTATGAAAACCTGAAATAA
TAAAAAGAGAAAAAACTAAAAA

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FIGURE 324

MQVSKRMLAGGVRSMFSPLLACWQPIILLVLGSLVSGSATGCPPRCECSAQDRAVLCHRRKCFVAVPEGIPTETRL
LDLGKNNRIKTLNQDEFASFPHLEELELNENIVSAVEPGAFFNNLNLRTLGRLSRNRLKLIPLGVFTGLSNLTKQDI
SENKIVILLDDYMFQDLNKLKSLVEGDNLDVYISHRAFSGLNSLEQLTLEKCNLTSTIPTALSHLHGLIVLRRLBL
NINAIIRDYSFKRLYRLKVLEISHWPLYLDTMTFNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPIS
TIEGSMHELLRLQEIQLVGGQLAVVEPYAFRGLNLYLRVLNVSGNQLTTLEESVFHSGVGNLETLILDSNPLACDC
RLWVFRRRWRNLNFRQQFTCATPEFVQGEKDFPDVLLPNYFTCCRARIQRKAQQVFVDEGHTVQFVCRADG
DPPPAILLWLSPRKHLVSAKSNGLTVFPDGTLEVRVYAQVQDNGTYLCIAANAGGNSMPAHLHVRSYSPDWPHQP
NKTFAFISNQFGEGEANSTRATVPFPFDIKTLIIATTMGFISFLGVVLFCLVLLFLWSRGKGNTHNIELEYVPR
KSDAGISSADAPRKFNMKMI

Important features:**Signal sequence:**

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345, 492-496,
505-509, 526-530, 542-546**Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353, 607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143, 262-268, 320-326,
344-350, 359-365, 493-499, 503-509, 605-611**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

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FIGURE 325

CCCACGCGTCCGCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGAG
GCAGGAGAGGAGGAGGTGGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGAGG
AGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAAGGAGAGAGGGACGAGGAGGAG
GAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAACGGAG
AGGAGGTGTGGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGAGTAGG
AAGATCAGGAGCTAGAGGGAGACTGGAGGGTTCCGGGAAAAGAGCAGAGGAAAAGAGGAAAGAC
ACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTGGCTGCTT
TGGCATTGGGGAAGTGGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCTCGAGGGAC
AGGGTCCCAGAAGGAGGGGACAGAGGAGCTGAGAGAGGGGGGCGAGGGCGTTGGCGAGGGGTCC
CTCGGAGGCCTCCTGGGATGGGGGCTGCAGCTCGTCTGAGCGCCCCGAGCGCTGGTACTC
TGGGCTGCACTGGGGGACGACGCTCACATCGGACCAGCACCTGACCCCGAGGACTGGTGGAGC
TACAAGGATAATCTCCAGGGAACCTTCGTGCCAGGGCCTCCTTTCTGGGGCTGGTGAATGCA
GCGTGGAGTCTGTGTGCTGTGGGGAAGCGGCAGAGCCCGTGGATGTGGAGCTGAAGAGGGTT
CTTTATGACCCCTTTCTGCCCCATTAAAGGCTCAGCACTGGAGGAGAGAAGCTCCGGGGAACC
TTGTACAACACCGGCCGACATGTCTCCTTCTGCTGCACCCCGACCTGTGGTCAATGTGTCT
GGAGGTCCCCTCCTTTACAGCCACCGACTCAGTGAAGTGCAGGCTGCTGTTTGGAGCTCGCGAC
GGAGCCGGCTCGGAACATCAGATCAACCACCAGGGCTTCTCTGCTGAGGTGCAGCTCATTAC
TTCAACCAGGAACCTACGGGAATTTACAGCGCTGCCTCCCGGGCCCCAATGGCCTGGCCATT
CTCAGCCTCTTTGTCAACGTTGCCAGTACCTCTAACCCTATTCCTCAGTCGCTCCTTAACCGC
GACACCATCACTCGCATCTCTACAAGAATGATGCCTACTTTCTTCAAGACCTGAGCCTGGAG
CTCCTGTTCCCTGAATCCTTCGGCTTCATCACCTATCAGGGCTCTCTCAGCACCCCGCCCTGC
TCCGAGACTGTCACTGGATCCTCATTGACCGGGCCCTCAATATCACCTCCCTTCAGATGCAC
TCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCTTCCAGAGCCTCAGCGGTAACAGC
CGGCCCTGCAGCCCTTGGCCACAGGGCACTGAGGGGCAACAGGAGCCCCCGGACCCCCGAG
AGGCGTGCCGAGGCCCCAATACCGCTGCATGTGGATGGTGTCCCCATGGTGCCTGAGAC
TCCCCTTCGAGGATTGCACCCGCCGCTCCTAAGCCTCCCCACAAGGCGAGGGGAGTTACCCCT
AAAACAAAGCTATTAAAGGGACAGAATACTTA

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FIGURE 326

MGAAARLSAPRALVLWAAALGAAAHIGFAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLCA
VGKRQSPVDVELKRVLYDPFLPPLRLSTGGKELRGTYNTGRHVSFLPAPRPVVNVSGGPLY
SHRLSELRLLEFGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSLFVN
VASTSNPFSLRLNDRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSETVTW
ILIDRALNITSQMHSRLRLSQNPFSQIFQSLSGNSRPLQPLAHRALRGNRDPRHPERRCRGP
NYRLHVDGVPHGR

Important features:**Signal peptide:**

Amino acids 1-23

Transmembrane domain:

Amino acids 177-199

N-glycosylation sites:

Amino acids 118-122;170-174;260-264

Eukaryotic-type carbonic anhydrases proteins:

Amino acids 222-271;128-165;45-93

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FIGURE 327

GGACTAATCTGTGGGAGCAGTTTATTCCAGTATCACCCAGGGTGCAGCCACACCAGGACTGTGTTGAAGGGTGT
TTTTTCTCTTTAAATGTAATACCTCCTCATCTTTCTCTTACACAGTGTCTGAGAACATTATACATTATAGATAA
GTAGTACATGGTGGATAACTTCTACTTTTAGGAGGACTACTCTCTCTGACAGTCTTAGACTGGTCTTCTACACT
AAGACACCA**AGA**AGGAGTATGTGCTCCTATTATTCCTGGCTTTGTGCTCTGCCAAACCCCTCTTTAGCCCTTAC
ACATCGCACTGAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATGATGATGATG
ATGATGATGAGGACAACCTCTCTTTTCCAAACAAGAGGCCAAGAAGCCATTTTTCATTGATCTGTTTCCAA
TGTGTCCATTTGGATGTCAGTGTCTATTACAGAGTTGTACATTGCTCAGATTAGGTTGACCTCAGTCCCAACCA
ACATTCCATTTGATACTCGAATGCTTGATCTTCAAAACAATAAAATTAAGGAAATCAAGGAAATGATTTTAAAG
GACTCACTTCACCTTTATGGTCTGATCCTGAACAACAACAGCTAACGAAGATTCACCCCAAAGCCTTCTAACCA
CAAAGAAGTTGCGAAGGCTGTATCTGTCCCACAATCAACTAAGTGAAATACCCTTAATCTTCCCAAAATCATTAG
CAGAATCAGAATTGATAAAATAAGTTAAGAAATACAAAGGACACATTCAAAGGAATGAATGCTTTACACG
TTTTGGAAATGAGTGCAAAACCCCTCTTGATAATAATGGGATAGAGCCAGGGGCATTTGAAGGGGTGACGGTGTCC
ATATCAGAATTGCGAAGCAAAACTGACCTCAGTTCCTAAAGGCTTACCACCAACTTTATTGGAGCTTCACCTAG
ATTATAATAAAATTTCAACAGTGGAACTTGAGGATTTTAAACGATACAAAGAACTACAAAGGCTGGGCCTAGGAA
ACAACAAATCACAGATATCGAAATGGGAGTCTTGCTAACATACCACGTGTGAGAGAAATACATTTGGAAAAACA
ATAAACTAAAAAAATCCCTTCAGGATTACCAGAGTTGAATACCTCCAGATAATCTTCTCTCATCTAATTCAA
TTGCAAGAGTGGGAGTAAATGACTTCTGTCCAAGTGCCAAAGATGAAGAAATCTTTATACAGTGCAATAAGTT
TATTCAACAACCCGGTGAATACTGGGAAATGCAACCTGCAACATTTCTGTTGTGTTTGGAGCAGATGAGTGTTC
AGCTTGGGAACCTTTGGAATG**AAA**TAATTAGTAATGGTAATGTCCATTTAATATAAGATTCAAAATCCCTACAT
TTGGAATACTTGAACCTCTATTATAATGGTAGTATTATATATACAAGCAAAATCTAATCTCAAGTGGTAAGTCC
ACTGACTTATTTTATGACAAGAAATTTCAACGGAAATTTGCCAAACTATTGATACATAAGGGGTTGAGAGAAACA
AGCATCTATTGCAGTTTCCTTTTTCGCTACAAATGATCTTACATAAAATCTCATGCTTGACCAATTCCTTCTTCAT
AACAAAAAGTAGATATTCCGTATTTAACACTTGTATCAAGCACATTTAAAAAGAACTGTACTGTAAATGG
AATGCTTGACTTAGCAAAATTTTGCTCTTTTCATTGCTGTGTAGAAAAACAGAATTAAACAAGACAGTAATGIGA
AGAGTGCAATTACACTATTCTTATTCTTTAGTAACCTGGGTAGTACTGTAATATTTTAAATCATCTTAAAGTATGA
TTTGATATAATCTTATTGAATTAACCTTATCATGTCTTAGAGCCCGTCTTATGTTTAAAACTAATTTCTTAAAA
TAAAGCCTTCAGATAAATGTTCAATTACCAACTTGATAAATGCTACPCATAAGAGCTGGTTTGGGGCTATAGCATAT
GCTTTTTTTTTTTAATTAATACCTGATTTAAAAATCTCTGTAAAAACGTGATAGTGTTCATATAAAATCTGTAACT
CGCATTTTAATGATCCCGTATTATAAGCTTTTAATAGCATGAAAAATTTGTAGGCTATATAAATGCACTTGCCACTCAA
CTCTAAGGAATATTTTGGAGATATCCCTTTGGAAGACCTTGCTTGAAGAGCCTGGACACTAACAAATCTACACC
AAATTTGTCTCTTCAAATACGTATGGACTGGATAACTCTGAGAAACACATCTAGTATAACTGAATAAGCAGAGCAT
CAAAATAAACAGACAGAAACCGAAAGCTCTATATAAATGCTCAGAGTCTCTTATGATTTCTTATTGGCATTCAA
CATATGTAATAATCAGAAAAACAGGAAATTTTCATTAAAAATATTGGTTTGAAT

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FIGURE 328

MKEYVLLLFALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDNSLFPTREPRS
HFFPFDLFEMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTS
LYGLILNNNKLTKIHPKAFLTTKKLRLLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDT
FKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLDYNKI
STVELEDFKRYKELQRLGLGNNKITDIENGLANIPRVREIHLNENKLLKIPSGLPFLKYLQI
IFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSVQLGNFGM

Important features:

Signal sequence.

amino acids 1-15

N-glycosylation site.

amino acids 281-285

N-myristoylation sites.

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

Leucine zipper pattern.

amino acids 154-176

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FIGURE 329

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGCA
TCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGCGCCCGCAGAAGACTTGTGT
TTGCCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCCTACCACCATGATCACTGGTGTGTT
CAGCATGCGCTTGTGGACCCAGTGGGCGTCTGACCTCGCTGGCGTACTGCCTGCACCAGCG
GCGGGTGGCCCTGGCCGAGCTGCAGGAGGCGGATGGCCAGTGTCCGGTCGACCGCAGCCGTGCT
GAAGTTGAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCCGCTCCC
GCTGGAGGAGCAGGTAGAGTGAACCCCAAGCTATTAGAGGTCCACCCCAAACCTCAGTTTGA
TTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCTCAATACCA
TGAGACCACTCAGGAGGAGTGGTGGGCGAGCTGACCAAGTGGGCATGCAGCAAAT
GTTTGCCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTCTTTACCAAC
CTTCAACCCACAGGAGGTCTTTATTGCTTCCACTAACATTTTTCGGAATCTGGAGTCCACCCG
TTGTTTGCTGGCTGGGCTTTTCCAGTGTGAGAAAGAGGCCATCATCATCCACACTGATGA
AGCAGATTGAGAAGTCTTGATATCCCAACTACCAAAGCTGCTGGAGCCTGAGGCAGAGAACCAG
AGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTGAAAAAGGTGAAGGA
CAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCTGGACAACGTGGCTGC
CGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTGCACGGATGATCGAACA
GAGAGCTGTGGACACATCCTTGACATACTGCCCAGGAAGACAGGGAAAGTCTTCAGATGGC
AGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGCCATGGACTCTGCCACTGC
CCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATGTGACCTTCATACCGCTCTT
AATGACCCTGGGGATTTTTGACCACAAAATGGCCACCGTTTGCTGTTGACCTGACCATGGAAC
TTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTATTACCACGGGAAGGAGCAGGT
GCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGTTCTTGAATGCCATGTCAGTTTA
TACCTTAAGCCCAGAAAAATACCATGCACCTCTGCTCTCAAACCTCAGGTGATGGAAGTTGGAAA
TGAAGAGTAACTGATTATATAAAGCAGGATGTGTTGATTTTAAAAATAAAGTGCCTTTATACAATG

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FIGURE 330

MITGVFSMRLWTFVGVLTSLAYCLHQRRVALAELQEADGGQCPVDRSLLKLMVQVVFRRHGARSPLKPLPLEEQVE
WNPQLLEVPQTQFDYTVTNLAGGPKPYSFYDSQYHETTLKGGMFAGQLTKVGMQMFALGERLRKNYVEDIFFL
SPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKEGPIIHTDEADSEVLVPNYQSCWSLRQRTGRRRQTASLQ
PGISEDLLKKVKDRMGIDSSDKVDFFILLDNVAAEQAHNLPSCPMLKRPFARMIEQRAVDTSLYILPKEDRESLQMA
VGPFLLHILESNNLLKAMDSATAPDKIRKLYLYAAHDVTFIPLMTLIGIFDHKWPPFAVDLTMLYQHLESKEWFVQ
LYYHGKEQVPRGCPDGLCPDLMFLNAMS VYTLSPKYHALCSQTQVMEVGNEE

Important features:

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

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FIGURE 331

CGAGGGCTTTTCGGGCTCCGGAATGGCACATGTGGGAATCCGAGTCTTGTTGGCTACAACATTTTCCCTTTCCCT
AACAAAGTTCTAACAGCTGTCTTAACAGCTAGTGATCAGGGGTTCTTCTTGCTGGAGAAGAAAGGCTCAGGGGCAG
AGCAGGGCACTCTCACTCAGGGTGACCAGCTCCCTGCCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGAT
GCAGCGGAGTGAGGGTGATGGAAGTCTAAAAATAGGAAGGAATTTGTGTGCATATCAGACTCTGGGAGCAGTTGA
CCTGGAGAGCCTGGGGGAGGGCCCTGCCTAACAGCTTTCAAAAACAGGAGCGACTTCCACTGGGCTGGGATAAG
ACGTGCCGGTAGGATAGGGAAGACTGGGTTTAGTCTTAATATCAAAATTGACTGGCTGGGTGAACCTCAACAGGCT
TTTAACTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAATAGAGATGCTTTGTAAAAATAAATTTTAA
AAAAAGCAAGTATTTTATAGCATAAAGGCTAGAGACCAAATAGATAACAGGATCCCTGAACATTCTTAAGAGG
GAGAAAGTATGTTAAAAATAGAAAACCAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGGACC
CTGGGTGAGCCAGCCCTCTTGCTCCTCCCGAAATATTTTTGGTCTGACCACTCTGCCTTGTTTTGCAGAA
TCATGTGAGGGCCAAACCGGGGAAGGTGGAGCAGATGAGCACACAGAGGCGGTCTCCTCACCGCGCCCTCTC
AGCATGGAACAGAGGCAGCCCTGGCCCGGGCCCTGGAGGTGGACAGCCGCTCTGTGGTCTGCTCTCAGTGGTC
TGGGTGCTGCTGCCCCCCAGCAGCGCGCATGCCTCAGTTCAGCACCTTCCACTCTGAGATCGTGACTGGACC
TTCAACCCTTGACCGTCCACCAAGGGACGGGGCCGTCTATGTGGGGGCCATCAACCGGGTCTATAAGCTGACA
GGCAACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCGGCCCTCATC
GTGCAGCCCTGCAGCGAAGTGCTCACCTTCACCAACAATGTCAACAAGCTGCTCATCTGACTACTCTGAGAAC
CGCTGCTGGCTGTGGGAGCCTCTACCAAGGGGTCTGCAAGCTGCTGCGCTGGATGACCTCTTCATCCTGGTG
GAGCCATCCCAACAAGAGGAGCACTACCTGTCCAGTGTCAACAAGACGGGCCCATGTACGGGGTGATTGTGCGC
TCTGAGGGTGAGGATGGCAAGCTCTTCATCGGCAGGCTGTGGATGGGAAGCAGGATTACTCCCGACCTGTCC
AGCCGGAAGCTGCCCGAGACCTGAGTCCCTCAGCCATGCTCGACTATGAGCTACACAGCATTTTGTCTCCTCT
CTCATAGATCCCTTCAGACACCTTGGCCCTGGTCTCCCACTTTGACATCTTACATCTACGGCTTTGCTAGT
GGGGGCTTTGTCTACTTTCTCACTGTCCAGCCGAGACCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTC
TTCTACACCTCAGCATCGTGCAGCTCTGCAAGGATGACCCCAAGTTCCACTCATAGTGTCCCTGCCCTTCGGC
TGCACCCGGGCGGGGTGGAATACCGCCTCTGCAGGCTGCTTACCTGGCCAAGCTGGGGACTCACTGGCCAG
GCCTTCATATACACAGCCAGGACGATGTACTCTTTGCCATCTTCTCCAAGGGCAGAAGCAGTATCACCAACCG
CCCAGTACTCTGCCCTGTGTGCCCTTCCCTATCCGGGCCATCAACTTCAGATCAAGGAGCGGCTGCAGTCCTGC
TACCAGGGCGAGGGCAACCTGGAGCTCAACTGGCTGCTGGGAAGGACGTCAGTGCACGAAGGCGCTGTCCCC
ATCGATGATAACTCTGTGGACTGGACATCAACCAGCCCTGGGAGGCTCAACTCCAGTGGAGGGGCTGACCTGT
TACACCACAGCAGGGACCGCATGACCTCTGTGGCTCCTACGTTTACAACGGCTACAGCGTGGTTTTTGTGGGG
ACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTCAGATGCTCCAATGCCATTACCTCCTCAGCAAA
GAGTCCCTCTTGAAGGTAGCTATTTGGTGGAGATTTAACTATAGGCACTTTATTTCTTGGGGAACAAGGGTGA
AATGGGAGGTAAAGAGGGTTAATTTTGTGACTTAGCTTCTAGTACTTCCCTCAGCCATCAGTCATGGGTAT
GTAAGGAATGCAAGCGTATTTCAATATTTCCAAACTTTAAGAAAAAACTTTAAGAAGGTACATCTGCAAAAGCAAA

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FIGURE 332

MGTLGQASLFAPPGNYFWSDHSA LCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWPR
ALEVD SRSVVLSSVVVLLAPPAAGMPQFSTFHSEN RDWTFNHLTVHQGTGAVYVGAINRVYK
LTGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKLLIIDYSENRLLAGGS LYQG
VCKLLRLDDLFI LVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDYFPTL
SSRKLPRDPFESSAMLDYELHSD FVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYELTVQPE
TPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKPGDSL AQ
AFNITSQDDVLF AIFSKGQKQYHHPDDSALCAFP IRAINLQIKERLQSCYQGE GNLELNWLL
GKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNGYSVVFVGT
KSGK LKKVRVYEFRCSNAIHL LSKESLLEGSYWWRFNYRQLYFLGEOR

Important features:**Signal sequence:**

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534**N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

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FIGURE 333

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCCAGCCTGTAACCTGTGCCCTACACCACGCCAGG
CCCCCCCAGAGCCCTCACCACGCTGGGCGCCCCAGAGCCCACACCATGCCGGGGACCTACGC
TCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGGCCCTGAT
GCGGGACTTCCCGCTCGTGGACGGCCACAACGACCTGCCCTTGGTCCTAAGGCAGGTTTACCA
GAAAGGGCTACAGGATGTTAACCTGCGCAATTTCAGCTACGGCCAGACCAGCCTGGACAGGCT
TAGAGATGGCCTCGTGGGCGCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCAGGACCG
GGATGCCCTGCGCCTCACCTGGAGCAGATTGACCTCATACGCCCATGTGTGCCCTCCTATTCT
TGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCCTGCGTCAT
CGGTGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTTTACATGCT
GGGAGTGCGCTACCTGACGCTCACCCACACCTGCAACACACCCTGGGCAGAGAGCTCCGCTAA
GGGCGCTCCACTCCTTCTACAACAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGTGGC
AGAAATGAACCGCTGGGCATGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCG
GGCCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCCACTCGGCTGCCCGGGGTGTGTGCAA
CAGTGCTCGGAATGTTCTGTGATGACATCCTGCAGCTTCTGAAGAAGAACGGTGGCGTCGTGAT
GGTGTCTTTGTCCATGGGAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGA
TCACTTCGACCACATCAAGGCTGTATTGGATCCAAGTTCATCGGGATTGGTGGAGATTATGA
TGGGGCCGGCAAATTCCTCAGGGGCTGGAAGACGTGTCCACATACCCGGTCTGATAGAGGA
GTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCTTCGTGGAAACCTGCTGCG
GGTCTTCAGACAAGTGGAAGGTACAGGAAGAAAACAATGGCAAAGCCCTTGGAGGACAA
GTTCCCGGATGAGCAGCTGAGCAGTTCTGCCACTCCGACCTCTCACGTCTGCGTCAGAGACA
GAGTCTGACTTCAGGCCAGGAAGTCACTGAGATTCCCATACACTGGACAGCCAAGTTACCAGC
CAAGTGGTCACTCTCAGAGTCCTCCCCCACATGGCCCCAGTCCTTGCAGTTGTGGCCACCTT
CCCAGTCCTTATTCTGTGGCTCTTGATGACCCAGTTAGTCCTGCCAGATGTCACTGTAGCAAGC
CACAGACACCCACAAAGTTCCTGTTGTGCAGGCACAAATATTTCTGAAATAAATGTTTT
GGACATAG

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FIGURE 334

MPGTYPSTTLSSPSTQGLQEQARALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYGO
TSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIRMCASYSELELVTSAKALNDTQ
KLACLIQVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGLTDF
GEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQLLKK
NGGVVMVSLSMGVIQCNPSPANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLEDVSTY
PVLIEELLSRGWSEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSSCHSDLS
RLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHMAPVLAVVATFPVLILWL

Important features:**N-glycosylation sites.**

amino acids 58-62, 123-127, 182-186, 273-277

N-myristoylation sites.

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

Renal dipeptidase active site.

amino acids 134-157

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FIGURE 336

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLEW
KKLGRSVSVFVYYQQTQLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTV
TLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSSQSTNSS
YTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVVALVIS
VCGLGVCYAQRKGYFSKETSFOKSNSSSKATTMSENVQWLTPVIPALWAAAAGGSRGQEF

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

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FIGURE 337

GGAGCGCCCTGGGTGTACAGCGCTCGGCTCCCGCGCAGCTCCGGCCGTGCGCAGCCTCGG
CACCTGCAGTCCGTGCGTCCCGCGGCTGGCGCCCTGACTCCGTCGCCGCCAGGGAGGGCCA
TGATTTCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGAGTG
CCCTGCGCCCCCTCGCGGGCCAGCTGCAACTGCACCTGCCCCCAACCGTTGCAGGCGG
TGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGGGGAGGTGTCTTCATCCC
AGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATCAGTGT
TGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCCATGCCCT
CCCGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCACAGCTGCT
CCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAACCTTAGAACTCA
ATGTACTGGTTCTCCAGCTCCTCCATCCTGCCGTCTCCAGGTGTGCCCATGTGGGGGCAA
ACGTGACCTTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACAGTGGGATCGGC
AGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCC
TCACCAACCTTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCACCAATGAGGTGGGCA
CTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTGTGCGGAG
CTGTTGTGGGTACCCTGGTTGSACTGGGGTTGCTGGCTGGGCTGGTCTCTTGTACCACCGCC
GGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCC
TGCCCTGGCCCAAGAGCTCAGACACAATCTCAAAGAATGGGACCCTTTCTCTGTCACTCCG
CACGAGCCCTCCGGCCACCCCATGGCCCTCCAGGCCTGGTGCATTGACCCCCACGCCCAGTC
TCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGATGGGGCCACCCCTCAACCAA
TATCCCCCATCCCTGGTGGGGTTTCTTCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA
TGGTGCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCACCACCTCATTGGCTAAAG
GATTTGGGGTCTCTCCTTCTCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATGGGAAAG
AGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTCTTTACTGTGGGAAAACCATCTCA
GTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGGAAAGTGGATCTGGAATTGGGAGGAGC
CTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAGCTACTACCAAGAGT
GAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGCCCCCTTGATCTGTACCCACCCCTAT
CTAACACCACCCCTTGGCTCCCACTCCAGCTCCCTGTATTGATATAACCTGTCAGGCTGGCTTG
GTTAGGTTTTTACTGGGGCAGAGGATAGGGAATCTCTTATTAATAAATAACATGAAATATGTGTT
GTTTTCATTGTCAAATTTAAATAAAGATACATAATGTTGTATGAAAAA